



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/727,898

DATE: 07/27/2004  
TIME: 13:04:45

Input Set : N:\Crf3\RULE60\10727898.raw  
Output Set: N:\CRF4\07272004\J727898.raw

## SEQUENCE LISTING

- 1 (1) GENERAL INFORMATION:  
 2     (i) APPLICANT: Williams, James A.  
        Thalley, Bruce S.  
 3     (ii) TITLE OF INVENTION: Multivalent Vaccine For Clostridium  
        Botulinum Neurotoxin  
 4     (iii) NUMBER OF SEQUENCES: 82  
 5     (iv) CORRESPONDENCE ADDRESS:  
     (A) ADDRESSEE: Medlen & Carroll  
     (B) STREET: 220 Montgomery Street, Suite 2200  
     (C) CITY: San Francisco  
     (D) STATE: California  
     (E) COUNTRY: United States of America  
     (F) ZIP: 94104  
 6     (v) COMPUTER READABLE FORM:  
     (A) MEDIUM TYPE: Floppy disk  
     (B) COMPUTER: IBM PC compatible  
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
 7     (vi) CURRENT APPLICATION DATA:  
 C--> 8         (A) APPLICATION NUMBER: US/10/727,898  
 C--> 9         (B) FILING DATE: 04-Dec-2003  
 10         (C) CLASSIFICATION: 424  
 11     (vii) PRIOR APPLICATION DATA:  
 12         (A) APPLICATION NUMBER: US/08/704,159  
 13         (B) FILING DATE:  
 14     (viii) ATTORNEY/AGENT INFORMATION:  
 15         (A) NAME: Ingolia, Diane E.  
 16         (B) REGISTRATION NUMBER: 40,027  
 17         (C) REFERENCE/DOCKET NUMBER: OPHD-02304  
 18     (ix) TELECOMMUNICATION INFORMATION:  
 19         (A) TELEPHONE: (415) 705-8410  
 20         (B) TELEFAX: (415) 397-8338  
 21 (2) INFORMATION FOR SEQ ID NO: 1:  
 22     (i) SEQUENCE CHARACTERISTICS:  
 23         (A) LENGTH: 24 base pairs  
 24         (B) TYPE: nucleic acid  
 25         (C) STRANDEDNESS: single  
 26         (D) TOPOLOGY: linear  
 27     (ii) MOLECULE TYPE: DNA (genomic)  
 28     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 29 41 GGAAATTTAG CTGCAGCATC TGAC  
 30 42 (2) INFORMATION FOR SEQ ID NO: 2:



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44      (i) SEQUENCE CHARACTERISTICS:
45          (A) LENGTH: 24 base pairs
46          (B) TYPE: nucleic acid
47          (C) STRANDEDNESS: single
48          (D) TOPOLOGY: linear
49      (ii) MOLECULE TYPE: DNA (genomic)
50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
51 TCTAGCAAAT TCGTTGTGT TGAA          24
53 (2) INFORMATION FOR SEQ ID NO: 3:
54      (i) SEQUENCE CHARACTERISTICS:
55          (A) LENGTH: 20 base pairs
56          (B) TYPE: nucleic acid
57          (C) STRANDEDNESS: single
58          (D) TOPOLOGY: linear
59      (ii) MOLECULE TYPE: DNA (genomic)
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
61 CTCGCATATA GCATTAGACC          20
63 (2) INFORMATION FOR SEQ ID NO: 4:
64      (i) SEQUENCE CHARACTERISTICS:
65          (A) LENGTH: 19 base pairs
66          (B) TYPE: nucleic acid
67          (C) STRANDEDNESS: single
68          (D) TOPOLOGY: linear
69      (ii) MOLECULE TYPE: DNA (genomic)
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
71 CTATCTAGGC CTAAAGTAT          19
73 (2) INFORMATION FOR SEQ ID NO: 5:
74      (i) SEQUENCE CHARACTERISTICS:
75          (A) LENGTH: 8133 base pairs
76          (B) TYPE: nucleic acid
77          (C) STRANDEDNESS: single
78          (D) TOPOLOGY: linear
79      (ii) MOLECULE TYPE: DNA (genomic)
80      (ix) FEATURE:
81          (A) NAME/KEY: CDS
82          (B) LOCATION: 1..8130
83      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
84 ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT          48
85 Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile
86      1           5           10           15
87 AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA          96
88 Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu
89      20           25           30
90 TAT AAT AAG TTA ACT ACA AAC AAT AAT GAA AAT AAA TAT TTG CAA TTA          144
91 Tyr Asn Lys Leu Thr Thr Asn Asn Glu Asn Lys Tyr Leu Gln Leu
92      35           40           45
93 AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT          192
94 Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr
95      50           55           60

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|     |   |      |
|-----|---|------|
| 96  | TCA AGC AGA AAT AGA GCA CTC TCT AAT CTA AAA AAA GAT ATA TTA AAA | 240  |
| 97  | Ser Ser Arg Asn Arg Ala Leu Ser Asn Leu Lys Lys Asp Ile Leu Lys |      |
| 98  | 65 70 75 80   |      |
| 99  | GAA GTA ATT CTT ATT AAA AAT TCC AAT ACA AGC CCT GTA GAA AAA AAT | 288  |
| 100 | Glu Val Ile Leu Ile Lys Asn Ser Asn Thr Ser Pro Val Glu Lys Asn |      |
| 101 | 85 90 95  |      |
| 102 | TTA CAT TTT GTA TGG ATA GGT GGA GAA GTC AGT GAT ATT GCT CTT GAA | 336  |
| 103 | Leu His Phe Val Trp Ile Gly Gly Glu Val Ser Asp Ile Ala Leu Glu |      |
| 104 | 100 105 110   |      |
| 105 | TAC ATA AAA CAA TGG GCT GAT ATT AAT GCA GAA TAT AAT ATT AAA CTG | 384  |
| 106 | Tyr Ile Lys Gln Trp Ala Asp Ile Asn Ala Glu Tyr Asn Ile Lys Leu |      |
| 107 | 115 120 125   |      |
| 108 | TGG TAT GAT AGT GAA GCA TTC TTA GTA AAT ACA CTA AAA AAG GCT ATA | 432  |
| 109 | Trp Tyr Asp Ser Glu Ala Phe Leu Val Asn Thr Leu Lys Lys Ala Ile |      |
| 110 | 130 135 140   |      |
| 111 | GTT GAA TCT TCT ACC ACT GAA GCA TTA CAG CTA CTA GAG GAA GAG ATT | 480  |
| 112 | Val Glu Ser Ser Thr Thr Glu Ala Leu Gln Leu Leu Glu Glu Ile     |      |
| 113 | 145 150 155 160   |      |
| 114 | CAA AAT CCT CAA TTT GAT AAT ATG AAA TTT TAC AAA AAA AGG ATG GAA | 528  |
| 115 | Gln Asn Pro Gln Phe Asp Asn Met Lys Phe Tyr Lys Lys Arg Met Glu |      |
| 116 | 165 170 175   |      |
| 117 | TTT ATA TAT GAT AGA CAA AAA AGG TTT ATA AAT TAT TAT AAA TCT CAA | 576  |
| 118 | Phe Ile Tyr Asp Arg Gln Lys Arg Phe Ile Asn Tyr Tyr Lys Ser Gln |      |
| 119 | 180 185 190   |      |
| 120 | ATC AAT AAA CCT ACA GTA CCT ACA ATA GAT GAT ATT ATA AAG TCT CAT | 624  |
| 121 | Ile Asn Lys Pro Thr Val Pro Thr Ile Asp Asp Ile Ile Lys Ser His |      |
| 122 | 195 200 205   |      |
| 123 | CTA GTA TCT GAA TAT AAT AGA GAT GAA ACT GTA TTA GAA TCA TAT AGA | 672  |
| 124 | Leu Val Ser Glu Tyr Asn Arg Asp Glu Thr Val Leu Glu Ser Tyr Arg |      |
| 125 | 210 215 220   |      |
| 126 | ACA AAT TCT TTG AGA AAA ATA AAT AGT AAT CAT GGG ATA GAT ATC AGG | 720  |
| 127 | Thr Asn Ser Leu Arg Lys Ile Asn Ser Asn His Gly Ile Asp Ile Arg |      |
| 128 | 225 230 235 240   |      |
| 129 | GCT AAT AGT TTG TTT ACA GAA CAA GAG TTA TTA AAT ATT TAT AGT CAG | 768  |
| 130 | Ala Asn Ser Leu Phe Thr Glu Gln Glu Leu Leu Asn Ile Tyr Ser Gln |      |
| 131 | 245 250 255   |      |
| 132 | GAG TTG TTA AAT CGT GGA AAT TTA GCT GCA GCA TCT GAC ATA GTA AGA | 816  |
| 133 | Glu Leu Leu Asn Arg Gly Asn Leu Ala Ala Ser Asp Ile Val Arg     |      |
| 134 | 260 265 270   |      |
| 135 | TTA TTA GCC CTA AAA AAT TTT GGC GGA GTA TAT TTA GAT GTT GAT ATG | 864  |
| 136 | Leu Leu Ala Leu Lys Asn Phe Gly Gly Val Tyr Leu Asp Val Asp Met |      |
| 137 | 275 280 285   |      |
| 138 | CTT CCA GGT ATT CAC TCT GAT TTA TTT AAA ACA ATA TCT AGA CCT AGC | 912  |
| 139 | Leu Pro Gly Ile His Ser Asp Leu Phe Lys Thr Ile Ser Arg Pro Ser |      |
| 140 | 290 295 300   |      |
| 141 | TCT ATT GGA CTA GAC CGT TGG GAA ATG ATA AAA TTA GAG GCT ATT ATG | 960  |
| 142 | Ser Ile Gly Leu Asp Arg Trp Glu Met Ile Lys Leu Glu Ala Ile Met |      |
| 143 | 305 310 315 320   |      |
| 144 | AAG TAT AAA AAA TAT ATA AAT AAT TAT ACA TCA GAA AAC TTT GAT AAA | 1008 |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 | Lys | Tyr | Lys | Lys | Tyr | Ile | Asn | Asn | Tyr | Thr | Ser | Glu | Asn | Phe | Asp | Lys |
| 146 |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     | 335 |
| 147 | CTT | GAT | CAA | CAA | TTA | AAA | GAT | AAT | TTT | AAA | CTC | ATT | ATA | GAA | AGT | AAA |
| 148 | Leu | Asp | Gln | Gln | Leu | Lys | Asp | Asn | Phe | Lys | Leu | Ile | Ile | Glu | Ser | Lys |
| 149 |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     |     | 350 |
| 150 | AGT | GAA | AAA | TCT | GAG | ATA | TTT | TCT | AAA | TTA | GAA | AAT | TTA | AAT | GTA | TCT |
| 151 | Ser | Glu | Lys | Ser | Glu | Ile | Phe | Ser | Lys | Leu | Glu | Asn | Leu | Asn | Val | Ser |
| 152 |     |     |     | 355 |     |     |     |     | 360 |     |     |     |     |     |     | 365 |
| 153 | GAT | CTT | GAA | ATT | AAA | ATA | GCT | TTC | GCT | TTA | GGC | AGT | GTT | ATA | AAT | CAA |
| 154 | Asp | Leu | Glu | Ile | Lys | Ile | Ala | Phe | Ala | Leu | Gly | Ser | Val | Ile | Asn | Gln |
| 155 |     |     |     | 370 |     |     |     |     | 375 |     |     |     |     |     |     | 380 |
| 156 | GCC | TTG | ATA | TCA | AAA | CAA | GGT | TCA | TAT | CTT | ACT | AAC | CTA | GTA | ATA | GAA |
| 157 | Ala | Leu | Ile | Ser | Lys | Gln | Gly | Ser | Tyr | Leu | Thr | Asn | Leu | Val | Ile | Glu |
| 158 | 385 |     |     |     | 390 |     |     |     | 395 |     |     |     |     |     |     | 400 |
| 159 | CAA | GTA | AAA | AAT | AGA | TAT | CAA | TTT | TTA | AAC | CAA | CAC | CTT | AAC | CCA | GCC |
| 160 | Gln | Val | Lys | Asn | Arg | Tyr | Gln | Phe | Leu | Asn | Gln | His | Leu | Asn | Pro | Ala |
| 161 |     |     |     |     | 405 |     |     |     | 410 |     |     |     |     |     |     | 415 |
| 162 | ATA | GAG | TCT | GAT | AAT | AAC | TTC | ACA | GAT | ACT | ACT | AAA | ATT | TTT | CAT | GAT |
| 163 | Ile | Glu | Ser | Asp | Asn | Asn | Phe | Thr | Asp | Thr | Thr | Lys | Ile | Phe | His | Asp |
| 164 |     |     |     |     | 420 |     |     |     | 425 |     |     |     |     |     |     | 430 |
| 165 | TCA | TTA | TTT | AAT | TCA | GCT | ACC | GCA | GAA | AAC | TCT | ATG | TTT | TTA | ACA | AAA |
| 166 | Ser | Leu | Phe | Asn | Ser | Ala | Thr | Ala | Glu | Asn | Ser | Met | Phe | Leu | Thr | Lys |
| 167 |     |     |     |     | 435 |     |     |     | 440 |     |     |     |     |     |     | 445 |
| 168 | ATA | GCA | CCA | TAC | TTA | CAA | GTA | GGT | TTT | ATG | CCA | GAA | GCT | CGC | TCC | ACA |
| 169 | Ile | Ala | Pro | Tyr | Leu | Gln | Val | Gly | Phe | Met | Pro | Glu | Ala | Arg | Ser | Thr |
| 170 |     |     |     |     | 450 |     |     |     | 455 |     |     |     |     |     |     | 460 |
| 171 | ATA | AGT | TTA | AGT | GGT | CCA | GGA | GCT | TAT | GCG | TCA | GCT | TAC | TAT | GAT | TTC |
| 172 | Ile | Ser | Leu | Ser | Gly | Pro | Gly | Ala | Tyr | Ala | Ser | Ala | Tyr | Tyr | Asp | Phe |
| 173 | 465 |     |     |     | 470 |     |     |     | 475 |     |     |     |     |     |     | 480 |
| 174 | ATA | AAT | TTA | CAA | GAA | AAT | ACT | ATA | GAA | AAA | ACT | TTA | AAA | GCA | TCA | GAT |
| 175 | Ile | Asn | Leu | Gln | Glu | Asn | Thr | Ile | Glu | Lys | Thr | Leu | Lys | Ala | Ser | Asp |
| 176 |     |     |     |     | 485 |     |     |     | 490 |     |     |     |     |     |     | 495 |
| 177 | TTA | ATA | GAA | TTT | AAA | TTC | CCA | GAA | AAT | AAT | CTA | TCT | CAA | TTG | ACA | GAA |
| 178 | Leu | Ile | Glu | Phe | Lys | Phe | Pro | Glu | Asn | Asn | Leu | Ser | Gln | Leu | Thr | Glu |
| 179 |     |     |     |     | 500 |     |     |     | 505 |     |     |     |     |     |     | 510 |
| 180 | CAA | GAA | ATA | AAT | AGT | CTA | TGG | AGC | TTT | GAT | CAA | GCA | AGT | GCA | AAA | TAT |
| 181 | Gln | Glu | Ile | Asn | Ser | Leu | Trp | Ser | Phe | Asp | Gln | Ala | Ser | Ala | Lys | Tyr |
| 182 |     |     |     |     | 515 |     |     |     | 520 |     |     |     |     |     |     | 525 |
| 183 | CAA | TTT | GAG | AAA | TAT | GTA | AGA | GAT | TAT | ACT | GGT | GGA | TCT | CTT | TCT | GAA |
| 184 | Gln | Phe | Glu | Lys | Tyr | Val | Arg | Asp | Tyr | Thr | Gly | Gly | Ser | Leu | Ser | Glu |
| 185 |     |     |     |     | 530 |     |     |     | 535 |     |     |     |     |     |     | 540 |
| 186 | GAC | AAT | GGG | GTA | GAC | TTT | AAT | AAA | AAT | ACT | GCC | CTC | GAC | AAA | AAC | TAT |
| 187 | Asp | Asn | Gly | Val | Asp | Phe | Asn | Lys | Asn | Thr | Ala | Leu | Asp | Lys | Asn | Tyr |
| 188 | 545 |     |     |     | 550 |     |     |     | 555 |     |     |     |     |     |     | 560 |
| 189 | TTA | TTA | AAT | AAT | AAA | ATT | CCA | TCA | AAC | AAT | GTA | GAA | GAA | GCT | GGA | AGT |
| 190 | Leu | Leu | Asn | Asn | Lys | Ile | Pro | Ser | Asn | Asn | Val | Glu | Glu | Ala | Gly | Ser |
| 191 |     |     |     |     | 565 |     |     |     | 570 |     |     |     |     |     |     | 575 |
| 192 | AAA | AAT | TAT | GTT | CAT | TAT | ATC | ATA | CAG | TTA | CAA | GGA | GAT | GAT | ATA | AGT |
| 193 | Lys | Asn | Tyr | Val | His | Tyr | Ile | Ile | Gln | Leu | Gln | Gly | Asp | Asp | Ile | Ser |

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|     |   |     |     |      |
|-----|---|-----|-----|------|
| 194 | 580   | 585 | 590 |      |
| 195 | TAT GAA GCA ACA TGC AAT TTA TTT TCT AAA AAT CCT AAA AAT AGT ATT |     |     | 1824 |
| 196 | Tyr Glu Ala Thr Cys Asn Leu Phe Ser Lys Asn Pro Lys Asn Ser Ile |     |     |      |
| 197 | 595   | 600 | 605 |      |
| 198 | ATT ATA CAA CGA AAT ATG AAT GAA AGT GCA AAA AGC TAC TTT TTA AGT |     |     | 1872 |
| 199 | Ile Ile Gln Arg Asn Met Asn Glu Ser Ala Lys Ser Tyr Phe Leu Ser |     |     |      |
| 200 | 610   | 615 | 620 |      |
| 201 | GAT GAT GGA GAA TCT ATT TTA GAA TTA AAT AAA TAT AGG ATA CCT GAA |     |     | 1920 |
| 202 | Asp Asp Gly Glu Ser Ile Leu Glu Leu Asn Lys Tyr Arg Ile Pro Glu |     |     |      |
| 203 | 625   | 630 | 635 | 640  |
| 204 | AGA TTA AAA AAT AAG GAA AAA GTA AAA GTA ACC TTT ATT GGA CAT GGT |     |     | 1968 |
| 205 | Arg Leu Lys Asn Lys Glu Lys Val Lys Val Thr Phe Ile Gly His Gly |     |     |      |
| 206 | 645   | 650 | 655 |      |
| 207 | AAA GAT GAA TTC AAC ACA AGC GAA TTT GCT AGA TTA AGT GTA GAT TCA |     |     | 2016 |
| 208 | Lys Asp Glu Phe Asn Thr Ser Glu Phe Ala Arg Leu Ser Val Asp Ser |     |     |      |
| 209 | 660   | 665 | 670 |      |
| 210 | CTT TCC AAT GAG ATA AGT TCA TTT TTA GAT ACC ATA AAA TTA GAT ATA |     |     | 2064 |
| 211 | Leu Ser Asn Glu Ile Ser Ser Phe Leu Asp Thr Ile Lys Leu Asp Ile |     |     |      |
| 212 | 675   | 680 | 685 |      |
| 213 | TCA CCT AAA AAT GTA GAA GTA AAC TTA CTT GGA TGT AAT ATG TTT AGT |     |     | 2112 |
| 214 | Ser Pro Lys Asn Val Glu Val Asn Leu Leu Gly Cys Asn Met Phe Ser |     |     |      |
| 215 | 690   | 695 | 700 |      |
| 216 | TAT GAT TTT AAT GTT GAA GAA ACT TAT CCT GGG AAG TTG CTA TTA AGT |     |     | 2160 |
| 217 | Tyr Asp Phe Asn Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Leu Ser |     |     |      |
| 218 | 705   | 710 | 715 | 720  |
| 219 | ATT ATG GAC AAA ATT ACT TCC ACT TTA CCT GAT GTA AAT AAA AAT TCT |     |     | 2208 |
| 220 | Ile Met Asp Lys Ile Thr Ser Thr Leu Pro Asp Val Asn Lys Asn Ser |     |     |      |
| 221 | 725   | 730 | 735 |      |
| 222 | ATT ACT ATA GGA GCA AAT CAA TAT GAA GTA AGA ATT AAT AGT GAG GGA |     |     | 2256 |
| 223 | Ile Thr Ile Gly Ala Asn Gln Tyr Glu Val Arg Ile Asn Ser Glu Gly |     |     |      |
| 224 | 740   | 745 | 750 |      |
| 225 | AGA AAA GAA CTT CTG GCT CAC TCA GGT AAA TGG ATA AAT AAA GAA GAA |     |     | 2304 |
| 226 | Arg Lys Glu Leu Leu Ala His Ser Gly Lys Trp Ile Asn Lys Glu Glu |     |     |      |
| 227 | 755   | 760 | 765 |      |
| 228 | GCT ATT ATG AGC GAT TTA TCT AGT AAA GAA TAC ATT TTT TTT GAT TCT |     |     | 2352 |
| 229 | Ala Ile Met Ser Asp Leu Ser Ser Lys Glu Tyr Ile Phe Phe Asp Ser |     |     |      |
| 230 | 770   | 775 | 780 |      |
| 231 | ATA GAT AAT AAG CTA AAA GCA AAG TCC AAG AAT ATT CCA GGA TTA GCA |     |     | 2400 |
| 232 | Ile Asp Asn Lys Leu Lys Ala Lys Ser Lys Asn Ile Pro Gly Leu Ala |     |     |      |
| 233 | 785   | 790 | 795 | 800  |
| 234 | TCA ATA TCA GAA GAT ATA AAA ACA TTA TTA CTT GAT GCA AGT GTT AGT |     |     | 2448 |
| 235 | Ser Ile Ser Glu Asp Ile Lys Thr Leu Leu Asp Ala Ser Val Ser     |     |     |      |
| 236 | 805   | 810 | 815 |      |
| 237 | CCT GAT ACA AAA TTT ATT TTA AAT AAT CTT AAG CTT AAT ATT GAA TCT |     |     | 2496 |
| 238 | Pro Asp Thr Lys Phe Ile Leu Asn Asn Leu Lys Leu Asn Ile Glu Ser |     |     |      |
| 239 | 820   | 825 | 830 |      |
| 240 | TCT ATT GGG GAT TAC ATT TAT TAT GAA AAA TTA GAG CCT GTT AAA AAT |     |     | 2544 |
| 241 | Ser Ile Gly Asp Tyr Ile Tyr Tyr Glu Lys Leu Glu Pro Val Lys Asn |     |     |      |
| 242 | 835   | 840 | 845 |      |

**VERIFICATION SUMMARY**

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Input Set : N:\Crf3\RULE60\10727898.raw

Output Set: N:\CRF4\07272004\J727898.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:2911 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32  
L:7982 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=82